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| Novartis Vaccines and Diagnostics, Inc. Corporate Intellectual Property P.O. BOX 8097 EMERYVILLE, CA 94662-8097 | | | EXAMINER DAVIS, MINH TAM B | |
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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary

Application No.

10/540,898

Applicant(s)

MORRIS ET AL.

Examiner

MINH-TAM DAVIS

Art Unit

1642

Period for Reply -- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 14 October 2008.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 49, 56-63, 66-72 and 75-86 is/are pending in the application.
- 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 49, 56-63, 66-72 and 75-86 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
 2. ☐ Certified copies of the priority documents have been received in Application No. _____.
 3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892)
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☒ Information Disclosure Statement(s) (PTO/SB/808)
Paper No(s)/Mail Date 10/25/07.
- 4) ☐ Interview Summary (PTO-413)
Paper No(s)/Mail Date _____.
- 5) ☐ Notice of Informal Patent Application
- 6) ☐ Other: _____

DETAILED ACTION

Applicant's election with traverse of group K, claims 49, 56-63, 66-74, a method for detecting colon cancer, using a combination of components of proteasome C7-I, SEQ ID NO:150, SEQ ID NO:152, and SEQ ID NO:154 in the reply filed on 10/14/08 is acknowledged.

The traversal is on the ground(s) that searching all three claimed cancers would not constitute a serious burden.

This is not found to be persuasive because it would be a serious burden to search for diagnosis of all three claimed cancers. Diagnosing different cancers requires different target cancer population, which has different properties. Further, there may be articles describing detection of one type of cancer, without mentioning detection of another cancer, using the same product. As such, it would be a serious burden to search for diagnosis of all three claimed cancers.

The requirement is still deemed proper and is therefore made FINAL.

After review and reconsideration, a method for diagnosing colon cancer, using a single nucleic acid SEQ ID NO:150, SEQ ID NO:152, or SEQ ID NO:154 is rejoined with a method for diagnosing colon cancer, using a combination of SEQ ID NO:150, SEQ ID NO:152, and SEQ ID NO:154.

Applicant adds new claims 75-86.

Accordingly, group K, claims 49, 56-63, 66-72, 75-86, diagnosis of colon cancer, by detecting the level of the nucleic acid SEQ ID NO:150, SEQ ID NO:152, and/or SEQ ID NO:154, are examined in the instant application.

The embodiment of claims 49, 56-63, 66-72, 75-86, as drawn to: 1) a method for diagnosis of colon cancer, by detecting the level of the protein encoded by the nucleic acid SEQ ID NO:150, SEQ ID NO:152, and/or SEQ ID NO:154, and 2) a method for diagnosis of stomach or prostate cancer, has been withdrawn from consideration as being drawn to non-elected invention.

Claim Rejections - 35 USC § 112, Second Paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 49, 61-63, 66-71, 85-86 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

1. Claims 49, 86 are indefinite, because it is not clear in claim 49 that the individual is “unaffected” by what.
2. Claims 49, 86 are indefinite, because although it is well known that a gene encodes a polypeptide, it is not clear in claim 49 how a gene “encodes” a nucleic acid sequence.
3. Claims 61-63, 66-71, 85-86 are indefinite, because it is not clear in claim 61, the “differential expression” in a patient sample is as compared to what.

Claim Rejections - 35 USC § 112, First Paragraph, Written Description

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it

pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claim 85 is rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The specification discloses that SEQ ID NO:150, SEQ ID NO:152 and SEQ ID NO: 154 are components of proteasome C7-I and encode a threonine endopeptidase. The specification however **does not disclose which portions of SEQ ID NO:150, SEQ ID NO:152 and SEQ ID NO: 154 are responsible for the threonine endopeptidase activity.**

The art does not disclose structure of 95% or 98% variants of SEQ ID NO:150, SEQ ID NO:152 and SEQ ID NO: 154, which variants have the threonine endopeptidase activity.

Although drawn to DNA arts, the findings in University of California v. Eli Lilly and Co., 119 F.3d 1559, 43 USPQ2d 1398 (Fed. Cir. 1997) and Enzo Biochem, Inc. V. Gen-Probe Inc. are relevant to the instant claims. The Federal Circuit addressed the application of the written description requirement to DNA-related inventions in University of California v. Eli Lilly and Co., 119 F.3d 1559, 43 USPQ2d 1398 (Fed. Cir. 1997). The court stated that “[a] written description of an invention involving a chemical genus, like a description of a chemical species, requires a precise definition, such as by structure, formula, [or] chemical name, of the claimed subject matter sufficient to distinguish it from other materials.” Id. At 1567, 43 USPQ2d at 1405. The court also stated that

a generic statement such as “vertebrate insulin cDNA” or “mammalian insulin cDNA” without more, is not an adequate written description of the genus because it does not distinguish the genus from others, except by function. It does not specifically define any of the genes that fall within its definition. It does not

define any structural features commonly possessed by members of the genus that distinguish them from others. One skilled in the art therefore cannot, as one can do with a fully described genus, visualize or recognize the identity of the members of the genus. A definition by function, as we have previously indicated, does not suffice to define the genus because it is only an indication of what the gene does, rather than what it is. Id. At 1568, 43 USPQ2d at 1406. The court concluded that “naming a type of material generally known to exist, in the absence of knowledge as to what that material consists of, is not a description of that material.” Id.

Finally, the court addressed the manner by which a genus of cDNAs might be described. “A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to the members of the genus, which features constitute a substantial portion of the genus.” Id.

The Federal Circuit has recently clarified that a DNA molecule can be adequately described without disclosing its complete structure. See Enzo Biochem, Inc. V. Gen-Probe Inc., 296 F.3d 1316, 63 USPQ2d 1609 (Fed. Cir. 2002). The Enzo court adopted the standard that □the written description requirement can be met by “show[ing] that an invention is complete by disclosure of sufficiently detailed, relevant identifying characteristicsi.e., complete or partial structure, other physical and/or chemical properties, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics.” Id. At 1324, 63 USPQ2d at 1613 (emphasis omitted, bracketed material in original).

The inventions at issue in Lilly and Enzo were DNA constructs per se, the holdings of those cases are also applicable to claims such as those at issue here. A disclosure that does not

adequately describe a product itself logically cannot adequately describe a method of using that product.

In this case, the specification does not describe the 95% or 98% variant polynucleotides in a manner that satisfies either the standards as shown in the example of Lilly or Enzo. The specification does not provide sufficient structure or common structure, other than SEQ ID NO:150, SEQ ID NO: 152 and SEQ ID NO: 154, to support the broad breath of the claimed genus. Nor is there any functional characteristics coupled with a known or disclosed correlation between structure and function. Although the specification discloses SEQ ID NO:150, SEQ ID NO: 152 and SEQ ID NO: 154, this does not provide a description of the 95% or 98% variants that would satisfy the standard as shown in the example of Enzo.

The specification also fails to describe the 95% or 98% variants, by the standards shown in the example in Lilly. The specification describes only SEQ ID NO:150, SEQ ID NO: 152 and SEQ ID NO: 154. Therefore, it necessarily fails to describe a “representative number” of such species. In addition, the specification also does not describe “structural features common to the members of the genus, which features constitute a substantial portion of the genus.”

The specification does not provide an adequate written description of the nucleic acid variants that is required to practice the claimed invention. Thus, the specification does not meet the 112, first paragraph written description requirement, and one of skill in the art would reasonably conclude that Applicant did not have possession of the claimed 95% or 98% variants at the time the invention was made. Since the specification fails to adequately describe the product for use in the claimed method, it also fails to adequately describe the claimed method.

Claim Rejections - 35 USC § 112, First Paragraph, Enablement

Claims 49, 56-63, 66-72, 75-86 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

To comply with the enablement requirement of 35 U.S.C. § 112, first paragraph, the specification must enable one skilled in the art to make and use the claimed invention without undue experimentation. The claims are evaluated for enablement based on the Wands analysis. Many of the factors regarding undue experimentation have been summarized in *In re Wands*, 858 F.2d 731, 8 USPQ2d 1400 (Fed.Circ.1988) as follows: (1) the nature of the invention, (2) the state of the prior art, (3) the predictability or lack thereof in the art, (4) the amount of direction or guidance present, (5) the presence or absence of working examples, (6) the quantity of experimentation necessary, (7) the relative skill of those in the art, and (8) the breadth of the claims.

The specification discloses that the claimed sequences can be used for detecting various cancers, one of which is colon cancer (p.7, last paragraph). The specification discloses that elevated level of cDNAs associated with cancer is detected using arrays (Example 3 on pages 174-177). The specification discloses that DNA from human colon tissue is extracted, and the sequence is detected using Southern blot (Example 4 on pages 177-178). The specification discloses that SEQ ID NO: 50, SEQ ID NO:152 and SEQ ID NO:154 encode a threonine endopeptidase, which are components of the proteasome C7-I (Table 130, on page 101).

There is, however, no data or objective evidence, however, that SEQ ID NO: 150, SEQ ID NO: 152 and /or SEQ ID NO:154 are differentially expressed in colon cancer tissue as compared to non-cancerous colon tissue. There is no data or objective evidence that patients who have a differential expression of SEQ ID NO: 150, SEQ ID NO:152 and /or SEQ ID NO:154 in their colon tissue as compared to the control non-cancerous colon tissue are predisposed to colon.

1. Claims 49, 56-63, 66-72, 75-86 are rejected under 35 U.S.C. 112, first paragraph, for lack of enablement for a method for **diagnosis of colon cancer**.

In the absence of objective evidence, one cannot determine whether the level of the nucleic acid SEQ ID NOs: 150, 152 and /or154 is different in colon cancer tissues as compared to non-cancerous colon tissues, because the level of expression of a polypeptide in cancer tissue is not predictable. It is well known in the art that not every gene in a cancer cell is affected in carcinogenesis, such as mutation or changes in expression as compared to normal control cells. For example, Stanton, P et al, 1994, Br J Cancer, 70: 427-433 teach that the level of expression of epidermal growth factor receptor (EGFR) cannot be predicted from cell lines or tumors (p.432, second column, last paragraph), and that from ten tumors from which the cell lines are derived, only two of the tumors display elevated levels of EGFR, BICR6 and BICR18 proteins (table V on page 430, and first column, last paragraph of page 430) In other words, not only the level EGFR, BICR6 and BICR18 proteins are the same as normal control in 8 tumors, the rest of other proteins in table V are not different from normal control in all ten tumors. Similarly, Ihle, C et al, 1999, J Steroid Biochem Mol Biol, 68: 189-195, teach that although the level of 5-alpha-reductase-1 is increased in prostate cancer tissue, the level of the isoform 5-alpha-reductase-2 is

the same as that of normal prostate (abstract). Abbaszadegan, M R, et al, 1994, Cancer Res, 54: 4676-4679, teach that the level of multidrug resistance-associated protein (MRP) detected in malignant hematopoietic cells is similar to the level found in normal hematopoietic cells (p.4678, second column, last 6 lines of second paragraph). Thus, since change in level of expression of a gene in a cancer tissue as compared to non-cancerous corresponding tissue is unpredictable, one cannot predict that the level of the nucleic acid SEQ ID NO: 150, SEQ ID NO: 152 and/or SEQ ID NO: 154 is different in colon cancer tissues as compared to non-cancerous colon tissues, and could be used in diagnosis of colon cancer.

Further, since it not clear what constitutes **“a normal tissue type”**, as recited in claim 49, **“a normal control”** as recited in claims 56, 60, **“a control”** as recited in claims 66, 68, or **“a normal colon tissue”** as recited in claim 67, which is not necessarily non-cancerous colon tissue, and the level of the claimed nucleic acid in which is not predictable, one would not know how to perform the claimed method.

In addition, since a difference in expression or **differential expression** encompasses either an increase or a decrease in the level of the claimed nucleic acid, it is not clear whether the level of claimed nucleic acid increases or decreases in colon cancer tissue as compared to non-cancerous colon tissue.

Moreover, one cannot predict that **any tissue type**, as recited in claim 49, or **any sample**, as recited in claim 61, could be used as a tested sample, because it is not necessarily cancerous, and even if said sample were cancerous, the claimed sample encompasses tissue other than colon cancer tissue to which colon cancer cells have **metastasized**. It is unpredictable that metastasized colon cancer cells still express the claimed sequences, because expression of a sequence could be

lost during the progression toward metastasis. For example, Kibel, AS et al, 2000, J urol, 164(1): 192-6 teach that gene expression in the chromosomal region 12p12-13 is different in primary and metastatic prostate cancer cells, and that inactivation in the chromosome region 12p12-13 occurs prior to metastasis. Similarly, Dong et al, 2000, Cancer Research, 60: 3880-3883, teach that deletion of a region in the chromosome 13q21 is associated with aggressive prostate cancer, as compared to less aggressive prostate cancer, such as primary prostate cancers that are not yet differentiated (abstract, and figure 1 on page 3882). Zhau, HE, 1994, J Cell Biochem, Suppl 19: 208-216, teach expression of various biomarkers associated with prostate cancer progression. Zhau et al teach that in prostate cancer, PC-3N35 subclones which are cloned from primary and metastatic sites (lymph node, kidney and bone), show difference in the levels of protein expression of various markers, such as c-erbB, vimentin, ICAM-1, cytokeratin, collagen IV between the parental PC-3N35 clone and its metastatic subclones (p.209 and table 1) and that the subline derived from the metastatic site lymph node has a 12p:17q translocation, whereas the bone-derived subline contains an isochromosome 7q (p.211, first column, first paragraph). Ren, C et al, 1998, Cancer Res, 58(6): 1285-90, teach a loss of expression of lysyl oxidase mRNA during progression to metastasis. Gingrich, JR et al, 1996, Cancer res, 56(18): 4096-4102 teach a loss of normal E-cadherin expression as primary tumors become less differentiated and metastasize. Russo, V et al, 1995, Int J Cancer, 64: 216-221, teach that analysis of multiple metastatic lesions and primary breast tumors show that in some cases the MAGE gene expression is lost during metastasis, but in some other cases, in metastasis nodes derived from MAGE-negative primary tumors, MAGE gene expression is detected (abstract, and table II on page 220). Thus in view of the above, one cannot predict that the claimed sequences are useful

for diagnosis of the presence in a subject of an metastatic colon cancer.

In addition, the specification further fails to identify and describe the 5' and 3' regulatory regions and untranslated regions essential to the function of the claimed invention, which are required since the claimed invention currently encompasses the **gene**. The art indicates that the structures of genes with naturally occurring regulatory elements and untranslated regions is empirically determined (Harris et al. J. of The Am Society of Nephrology 6:1125-33, 1995; Ahn et al. Nature Genetics 3(4):283-91, 1993; and Cawthon et al. Genomics 9(3):446-60, 1991). Therefore, the structure of these elements is not conventional in the art, and one cannot predict the structure of the claimed gene, comprising SEQ ID NO: 150, SEQ ID NO:152 or SEQ ID NO:154, as recited in claim 49.

Further, the method as claimed in claims 72, 86 would be non-specific. "**A complement**" is reasonably interpreted as full length or partial complement, wherein a partial complement needs to be complementary only to a few nucleotides of SEQ ID NO: 150, SEQ ID NO:152 or SEQ ID NO:154. In other words, the claimed method would detect unrelated sequences with unknown properties. Therefore, one cannot predict that a difference of at least 50% in the patient colon sample as compared to non-cancerous colon would be detected in the claimed method.

2. Further, proteasome component C7-I without being accompanied by a sequence identification encompasses proteasome C7-I variants, including the claimed 95% and 98% variants.

Even if SEQ ID NO: 150, SEQ ID NO:152 and/or SEQ ID NO:154 could be used for diagnosis of colon cancer, one cannot predict that its **variants**, including its **95% or 98% variant**, as recited in claims 56-58, 60-63, 66-70, 75-76, 78, 80-81, 83, 84-86 could be used for

diagnosis of colon cancer. It is well known in the art that variants of a sequence do not necessarily express at the same level as the corresponding wild type. For example, Schmid et al, 2001 (J comparative Neurology, 430(2): 160-71), teach that the variants flip/flop of the gene GluR are expressed at higher levels in neurons in the auditory brainstem, as compared to the wild type GluR-A and GluR-B, and that neurons in the central nucleus of the inferior colliculus express high levels of GluR-B flip but only low levels of the other receptor subunits. Conner et al, 1996 (Mol Brain Res, 42: 1-17), teach that full length trkB is found in the hippocampus in patients with Alzheimer's disease, but not in hippocampi of either normal age-matched individual or patients with Huntington's disease, and that truncated trkB is found in senile plaques in hippocampus and temporal lobe in both patients with Alzheimer's disease and Huntington's disease, but not in normal brains of age-matched individuals (page 8, item 3.1.2). Thus in view of the teaching in the art one cannot predict that the claimed variants including the 95% or 98% variants of SEQ ID NO: 150, SEQ ID NO:152 and/or SEQ ID NO:154 would differentially express in colon cancer tissue as compared to non-cancerous colon tissue.

3. Claim 60 is also rejected under 112, first paragraph, for lack of enablement for detection of **predisposition to or risk of colon cancer**. The specification provides neither guidance on nor exemplification of how to correlate the claimed differential expression of the proteasome C7-I nucleic acid with colon cancer risk. Tockman et al (Cancer Res., 1992, 52:2711s-2718s) teach considerations necessary in bringing a cancer biomarker (intermediate end point marker) to successful clinical application. Although the reference is drawn to biomarkers for early lung cancer detection, the basic principles taught are clearly applicable to the claimed invention. Tockman et al teaches that prior to the successful application of newly

described markers, research must validate the markers against acknowledged disease end points, establish quantitative criteria for marker presence/absence and **confirm marker predictive value in prospective population trials** (emphasis added) (see abstract). Early stage markers of carcinogenesis have clear biological plausibility as markers of preclinical cancer and **if validated** (emphasis added) can be used for population screening (p. 2713s, col 1). The reference further teaches that once selected, the sensitivity and specificity of the biomarker must be validated to a known (histology/cytology-confirmed) cancer outcome. The essential element of the validation of an early detection marker is the ability to test the marker on clinical material obtained from subjects monitored in advance of clinical cancer and link those marker results with subsequent histological confirmation of disease. This irrefutable link between antecedent marker and subsequent acknowledged disease is the essence of a valid intermediate end point marker (p. 2714, see Biomarker Validation against Acknowledged Disease End Points). Clearly, prior to the successful application of newly described markers, markers must be validated against acknowledged disease end points and the marker predictive value must be confirmed in prospective population trials (p. 2716s, col 2). Moreover, the need to perform validation studies when characterizing putative biomarkers is also confirmed by Oesterreich, S et al, 1996 (Clin Cancer Res, 2: 1199-1206, especially p. 1205, first column, last three lines of paragraph before last), who teach that false positive correlation can be obtained when using the univariate analysis to obtain a correlation of a marker with its prognostic value. Similarly, confirmation of prognosis ability of a marker protein is essential, in view of the teaching of Vandesompele J et al, 2003 (Oncogene, 22(3): 456-60). Vandesompele et al teach that the reported prognosis power of Id-2 expression in neuroblastoma cannot be confirmed, wherein Id-2 is assumed to be a direct target

for MYCN protooncogene, the amplification of which is correlated with highly aggressive neuroblastoma. Thus without validation of the claimed method, one cannot predict that the claimed differential expression of the proteasome C7-I nucleic acid indicates predisposition to or risk of colon cancer.

MPEP 2164.03 teaches that “the amount of guidance or direction needed to enable the invention is inversely related to the amount of knowledge in the state of the art as well as the predictability of the art. In re Fisher, 427 F.2d 833, 839, 166 USPQ 18, 24 (CCPA 1970). The amount of guidance or direction refers to that information in the application, as originally filed, that teaches exactly how to make or use the invention. The more that is known in the prior art about the nature of the invention, how to make, and how to use the invention, and the more predictable the art is, the less information needs to explicitly stated in the specification. In contrast, if little is known in the prior art about the nature of the invention and the art is unpredictable, the specification would need more detail as how to make and use the invention in order to be enabling.”

Given the above unpredictability, and in view of the complex nature of the invention, a lack of sufficient disclosure in the specification, and little is known in the art concerning the claimed invention, there would be an undue quantity of experimentation required for one of skill in the art to practice the claimed invention, that is commensurate in scope of the claims.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

Claims 61-63, 66-67, 69, 83, 86 are rejected under 35 U.S.C. 102(e) as being anticipated by Tang et al (US20030219745A1, filed on April, 11, 2002).

Claims 61-63, 66-67, 69, 83, 86 are as follows:

61. (Currently amended) A method for diagnosing colon, stomach or prostate cancer comprising detecting differential expression of a proteasome component C7-I in a patient sample, wherein differential expression of proteasome component C7-I indicates that the patient has colon cancer.

62. (Currently amended) The method of claim 61 wherein differential expression is detected by measuring the level of a proteasome component C7-I expression product.

63. (Previously presented) The method of claim 62 wherein the expression product is mRNA.

66. (Previously presented) The method of claim 62 wherein the level of a proteasome component C7-I expression product in the patient sample is compared to a control.

67. (Previously presented) The method of claim 66 wherein the control comprises normal colon tissue.

69. (Currently amended) The method of claim 61 wherein differential expression is detected by measuring the level of a proteasome component C7-I expression product said expression product comprising a nucleotide sequence at least 95% identical to SEQ ID NO: 154.

83. (New) The method of claim 61 wherein differential expression is detected by measuring the level of a proteasome component C7-I expression product at least 98% identical to SEQ ID NO:154.

86. (New) The method of any one of claims 49, 56, 61 or 72 wherein the cancer is colon cancer.

A proteasome component C7-I without being accompanied by a sequence identification encompasses proteasome C7-I variants, including the claimed 95% and 98% variants.

Tang et al teach a sequence, SEQ ID NO:124, which is 98% similar to the claimed SEQ ID NO:154, as shown by sequence similarity search (MPSRCH search result, 2008, us-10-540-898-154.rnbpbm, result 6, pages 1-2). Tang et al teach that the polynucleotide is useful for diagnosis of cancer, and that an increase in the level of the polynucleotide indicates ongoing cancer (para 211). One of the cancers cited by Tang et al is colon cancer (para 212).

Although the reference does not explicitly teach that the sequence is a proteasome component C7-I, however, the claimed sequence appears to be the same as the prior art sequence. The office does not have the facilities and resources to provide the factual evidence needed in order to establish that the product of the prior art does not possess the same material, structural and functional characteristics of the claimed product. In the absence of evidence to the contrary, the burden is on the applicant to prove that the claimed product is different from those taught by the prior art and to establish patentable differences. See *In re Best* 562F.2d 1252, 195 USPQ 430 (CCPA 1977) and *Ex parte Gray* 10 USPQ 2d 1922 (PTO Bd. Pat. App. & Int. 1989).

Because the method of the prior art comprises the same method steps as claimed in the instant invention using the same composition, the claimed method is anticipated because the

method will inherently lead to the claimed effects. See Ex parte Novitski 26 USPQ 1389 (BPAI 1993).

Conclusion

No claims are allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to MINH-TAM DAVIS whose telephone number is 571-272-0830. The examiner can normally be reached on 9:00 AM-5:30 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, LARRY HELMS can be reached on 571-272-0832. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

MINH TAM DAVIS

November 17, 2008

/Larry R. Helms/
Supervisory Patent Examiner, Art Unit 1643

MPSRCH search result, 2008, us-10-540-898-154.rnpsbm, result 6, pages 1-2

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RESULT 6
US-10-120-988-124
; Sequence 124, Application US/10120988
; Publication No. US20030219745A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Ren, Peiyan
; APPLICANT: Wang, Dunrui
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. US20030219745A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 802CON
; CURRENT APPLICATION NUMBER: US/10/120,988
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/774,528
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 124
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(673)
US-10-120-988-124

Query Match          98.7%; Score 747.4; DB 8; Length 787;
Best Local Similarity 99.2%; Pred. No. 2.8e-240;
Matches 751; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1  GGCAGCCATCTCGCCGCTGAGACAGCAAGTGTGCGGATCCGACGGGCGAGCCGTGCGATGTT 60
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      1  GGCAGGAGGCTCGCCGCTGAGACAGCAAGTGTGCGGATCCGACGGGCGAGCCGTGCGATGTT 60

Qy      61  GTCTCTCAGCCCATGTATTTCGGCTGCTGGCAGAGACTTGGGGATGGAACCGCAGCAGAG 120
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      61  GTCTCTCAGCCCATGTATTTCGGCTCTCTGCGAGAGACTTGGGGATGGAACCGCAGCAGAG 120

Qy      121  CGCGGGCCCTTTGCGAGCTGCGGATTTTCGCCCTACGTTTTCAACGGAGGAACAGACAAAAA 180
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      121  CGCGGGCCCTTTGCGAGCTGCGGATTTTCGCCCTACGTTTTCAACGGAGGAACAGACAAAAA 180

Qy      181  AGTCATTGGAATGCAAGCGGTTTTTCATGAGAGACTGTCTTACGCTGACAAAGATTATTGAAGC 240
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      181  AGTCATTGGAATGCAAGCGGTTTTTCATGAGAGACTGTCTTACGCTGACAAAGATTATTGAAGC 240

Qy      241  AAGACTAAAGATGTATTAAGCATTCCCAATAATAAGGCGATGACTACGGGGGCAATTGCTGC 300
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      241  AAGACTAAAGATGTATTAAGCATTCCCAATAATAAGGCGATGACTACGGGGGCAATTGCTGC 300

Qy      301  AATGCTGTCTCAAACTCTGTATTCAAGGCGCTTCTTTCCATACATATGTTTCAACATCAT 360
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      301  AATGCTGTCTCAAACTCTGTATTCAAGGCGCTTCTTTCCATACATATGTTTCAACATCAT 360

Qy      361  CGGTGGACTTGTATGAAGAAGAAAGGGGCTGTATACAGCTTTGATCCAGTAGGGTCTTAA 420
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      |||||||
Db      361  CGGTGGACTTGATGAAGAAGGAAGGGGGCTGTATACAGCTTTGATCCAGTAGGGTCTTA 420
Qy      421  CCAGAGAGACTTCCTTCAGGCTGGAGGCTCAGCAAGTGCCATGCTACAGCCCTGCTTGA 480
Db      421  CCAGAGAGACTTCCTTCAGGCTGGAGGCTCAGCAAGTGCCATGCTACAGCCCTGCTTGA 480
Qy      481  CAACCAGGTTGGTTTTAAGAACATGCAGAAATGTGGAGCATGTTCCGGCTGTCTTGGACAG 540
      |||||||
Db      481  CAACCAGGTTGGTTTTAAGAACATGCAGAAATGTGGAGCATGTTCCGGCTGTCTTGGACAG 540
Qy      541  AGCCATGCGGCTGGTGAAAGATGTCTTTCATTTCTGCGGCTGAGAGAGATGTGTACACTGG 600
      |||||||
Db      541  AGCCATGCGGCTGGTGAAAGATGTCTTTCATTTCTGCGGCTGAGAGAGATGTGTACACTGG 600
Qy      601  GGACGCACTCCGGATCTGCATAGTGACCAAGAGGGCATCAGGGAGGAAACTGTTTCCTT 660
      |||||||
Db      601  GGACGCACTCCGGATCTGCATAGTGACCAAGAGGGCATCAGGGAGGAAACTGTTTCCTT 660
Qy      661  AAGGAAGGACTGATCTGTGTGCTCTTATCACCAATCAGTTCAGACCTGGTTGATTTTGTA 720
      |||||||
Db      661  AAGGAAGGACTGATCTGTGTGCTCTTATCACCAATCAGTTCAGACCTGGTTGATTTTGTA 720
Qy      721  CTTTGGAAGTGTACCTTGGATGTTTTTGTATTATAA 757
      |||||||
Db      721  CTTTGGAAGTGTACCTTGGATGTTTTTGTATTATAA 757
  
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